

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 27, 2002, 12:08:08 ; Search time 3647.7 Seconds
(without alignments)
12199.320 Million cell updates/sec

Title: US-09-476-202a-1

Perfect score: 3297
Sequence: 1 tttaatcatggaatttca.....gttaagcaaccgccacca 3297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estchum:*
3: em_estcin:*
4: em_estclu:*
5: em_estcov:*
6: em_estdpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_lnv:*
15: em_gss_pln:*
16: em_gss_vrtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	249.8	7.6	439	9	AA515728 ng70f04.s
2	248.6	7.5	461	12	B65075 CIT-HSP-201
3	246.2	7.5	711	12	AQ415030 RPCI-11-2
4	244.4	7.4	386	9	AL079734 DKEZP434H
5	244.2	7.4	639	12	AQ377619 RPCI11-16
6	241	7.3	676	12	AG183410 Pan t1rog1
7	240.8	7.3	642	12	B59854 CIT-HSP-345
8	240.2	7.3	1655	11	BC022315 Homo sapi
9	239.8	7.3	661	10	BC927980 HNC45-1-G
10	239.2	7.3	521	9	AW970571 EST382652
11	239.2	7.3	669	12	AG156412 Pan t1rog1
12	239.2	7.3	897	12	AQ746057 HS_2277_A
13	239	7.2	397	9	AW020150 d105809.Y
14	238.2	7.2	614	12	AQ627870 CITBI-E1-
15	238.2	7.2	827	9	AV755654 AV755654
16	238	7.2	673	12	AG046383 Pan t1rog1
17	237.8	7.2	782	9	AL598828 DKEZP313L

18	237.6	7.2	649	12	AA080891 CIT-HSP-2
19	237.4	7.2	678	12	AQ387027 RPCI11-15
20	237.2	7.2	739	12	AQ200209 RPCI11-45
21	237	7.2	659	12	AG161184 Pan t1rog1
22	237	7.2	671	12	AQ311090 CITBI-E1-
23	236.8	7.2	437	10	BF724699
24	236.8	7.2	437	10	BF725884
25	236.8	7.2	667	12	AG156377 Pan t1rog1
26	236.6	7.2	635	12	AG154911 Pan t1rog1
27	236.4	7.2	530	9	AW798093 CM0-UM004
28	236.4	7.2	530	10	BF985049
29	236.4	7.2	393	10	BF805088 IL5-C1015
30	236.2	7.2	410	9	AA568314 n1f5c01.s
31	236.2	7.2	415	9	AA515048
32	236.2	7.2	556	9	AW970940 EST383023
33	236.2	7.2	674	12	AG123283
34	236	7.2	315	9	AW591754
35	236	7.2	836	12	AQ781745
36	235.8	7.2	562	12	AQ792364
37	235.6	7.1	365	9	A1049709 an37a09.x
38	235.6	7.1	484	9	AA410788
39	235.6	7.1	510	12	AQ534099 RPCI-11-3
40	235.6	7.1	597	9	AV762633
41	235.6	7.1	935	10	BF968880 602270854
42	235.4	7.1	413	9	AA714011
43	235.4	7.1	454	12	AQ268452 RPCI11-69
44	235.2	7.1	586	9	AV647713
45	235.2	7.1	753	10	B6567646 602586417

ALIGNMENTS

RESULT 1
AA515728 439 bp mRNA linear EST 19-AUG-1997
ng70f04.s1 NCL_CGAP_Lip2 Homo sapiens CDNA clone IMAGE:940159
LOCUS
DEFINITION
Similar to contains Alu repetitive element; contains element PTR5
repetitive element; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AA515728.1 GI:2255328
EST.
human.
Homo sapiens

REFERENCE

AUTHORS
TITLE
NCL-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizan, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bhrp/image/image.html
Insert Length: 634 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 358.
Location/Qualifiers

FEATURES

source

1. 439
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:940159"
/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
/note="Vector: pAMP10; mRNA made from liposarcoma, CDNA

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: mcdams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html
Seq primer: 77

Class: BAC ends.

FEATURES

Source

Location/Qualifiers

1..642

/organism="Homo sapiens"

/db_xref="GDB:5363319"

/db_xref="taxon:9606"

/clone="345H13"

/clone_lib="CIT-HSP"

/sex="Male"

/cell_type="Sperm"

/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"

BASE COUNT 171 a 121 c 180 g 170 t

ORIGIN

Query Match

Best Local Similarity 7.3%; Score 240.8; DB 12; Length 642;
Pred. No. 4.8e-25;

Matches 272; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1723 aaaaatcaggcttgctggtgcgtgctcatgcttataatcccaagcattggagagc 1782

Db 40 AAAAAATAGTTGTTGGCCGGGACAGTGGCTCATGCTGTAAATCCAGCATTTGGGAGGC 99

QY 1783 cgaatgagcgtatccccgagagtcagagattgtagccagctggcacaactgtgga 1842

Db 100 TAAAGCAGATGATCACTCGAGAGTCAAGAGTTCAGACCAAGCTGGCCAACTGGTGA 159

QY 1843 ccccatcttaccataataaattagccggcagtggtgctgcaactgttaacc 1902

Db 160 CCCCATCTCTACTAAATAATACAAATATAGCTGGGGGTGGTGGCCCTGTATCC 219

QY 1903 agctacttgggaagctgagagcaagaatcgcttgaacccagagagagattgca 1962

Db 220 AACTACTCGGAGGCTGAGAGCAGGAATCGCTTGAACCCAGAGAGCGAGTGTGAGTG 279

QY 1963 agctagatcggtcgctgcaactcagcctcagcaacagagcgagacatcctca 2022

Db 280 AGCCGAGATTGTGCCACCTGCACTTCAGCTTGGGTGACAGAGGAGACTCATTCTA 339

QY 2023 aaaaaaataaataaataaataa 2046

Db 340 AAAAAAAAAAAAAAAAAAGTAAGAA 363

RESULT 8

LOCUS BC022315 1655 bp mRNA linear HTC 04-FEB-2002

DEFINITION Homo sapiens, Interleukin 10, clone IMAGE:4691490, mRNA.

ACCESSION BC022315 GI:18490360

VERSION BC022315.1 GI:18490360

KEYWORDS HTC.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1655)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (01-FEB-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk

COMMENT Email: cgabs-remail.nih.gov

Tissue Procurement: CLOUTECH

CDNA Library Preparation: CLOUTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRL Plate: 36 Row: m Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 10835140
This clone has the following problem: frame shifted.

FEATURES

Source

Location/Qualifiers

1..1655

/organism="Homo sapiens"

/db_xref="LocusID:3586"

/db_xref="taxon:9606"

/clone="IMAGE:4691490"

/tissue_type="lung"

/clone_lib="NIH-MGC_77"

/lab_host="DH10B"

/note="Vector: pDNR-LIB"

BASE COUNT 481 a 376 c 363 g 435 t

ORIGIN

Query Match

Best Local Similarity 7.3%; Score 240.2; DB 11; Length 1655;

Matches 269; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1723 aaaaatcaggcttgctggtgcgtgctcatgcttataatcccaagcattggagagc 1782

Db 1190 AATTTGTTCTAAGCGCGGCGGCGGTGCTCACGCTGTAAATCCAGCATTTGGGAGGC 1249

QY 1783 cgaatgagcgtatccccgagagtcagagattgtagccagctggcacaactgtgga 1842

Db 1250 TAAAGGAGTGTGATCACTTGAAGTCTGAGATTCCTAACCAAGCTGTCAACATGGTGA 1309

QY 1843 ccccatcttaccataataaattagccggcagtggtgctgcaactgttaacc 1902

Db 1310 CCCCGTCTCTACTAAATAATACAAATATAGCCGGCATGTGGCGCACCTGTATCC 1369

QY 1903 agctacttgggaagctgagagcaagaatcgcttgaacccagagagcggaattgca 1962

Db 1370 AGCTACTTGGAGGCTGAGAGCAAGAAATGCTTGAACCCAGAGAGATGGAAGTTGAGTG 1429

QY 1963 agctagatcggtcgctgcaactcagcctcagcaacagagcgagacatcctca 2022

Db 1430 AGCTGATATCATGCCCCCTGTACTCAGCCTGGGTGACAGAGCAAGACTCTGTCAAAA 1489

QY 2023 aaaaaaataaataaataa 2039

Db 1490 ATRAAATATTAATAATANA 1506

RESULT 9

LOCUS BG927980 661 bp mRNA linear EST 06-NOV-2001

DEFINITION HNC45-1-G7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA

sequence.

ACCESSION BG927980

VERSION BG927980.1 GI:14322503

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	AUTHORS	TITLE	JOURNAL MEDLINE	COMMENT
1	(bases 1 to 661)	Mammalia: Eutheria; Primates; Catarrhini; Homiidae; Homo.		
1	Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Laik,M.M.	Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries	osteoarthritic Cartilage 9 (7), 641-653 (2001)	
21482651	Contact: Sanjay Kumar			
0W2109	GLASGOWKline			
709	Sweeeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA			
Tel:	610-270-7245			
Fax:	610-270-5598			
Email:	sanjay.kumar-1@sk.com			
Seq primer:	47,			
FEATURES	Location/Qualifiers			
source	1..661			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone_lib="HNC (Human Normal Cartilage)"			
	/tissue_type="cartilage"			
	/lab_host="E.coli DH10 B"			
	/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; Directional"			
BASE COUNT	186 a 127 c 174 g 174 t			
ORIGIN				
Query Match	7.3%: Score 239.8: DB 10; Length 661:			
Best Local Similarity	85.1%: Pred. No. 6.5e-25;			
Matches	268; Conservative 0; Mismatches 47; Indels 0; Gaps 0			
QY	1734 ttggctgggttgctggctgctatctatataatcccaagcacttggagagcgaatggcg 1793			
Db	135 TGGGCTGGGTCGGGTGCTTACACTCCGTAAATCCACACTTTGGGAGCGCAAGTGGGCA 194			
QY	1794 tttccctcgaagtcaggagttgtgtgacccagcctgtgccaacatggtgaaacccatctta 1853			
Db	135 GATCACTTGAGGTCAAGGAGTTTGAGAACCCGTGGCAACATGCTGAACCCGTCTCTCA 254			
QY	1854 ccaaaaataaanaattagccggcagatgtggcgatgtgacgttgtaatcccaagctactgg 1913			
Db	255 CTAAAAATATATAAATTTAGCTGCTGGTGGTGGCGTGCACATTGTAAATCCAGCTACTGGG 314			
QY	1914 aagctggagcgaagaatctgtcttgaccccaagagagaagtgtcagtgagctgagatgc 1973			
Db	315 AGCGTGAGGACAGAAATCACTTGAACCCGGAGACGACAGGTTCGAGTGAAGTGAATCA 374			
QY	1974 ttgccttgacatccgcagcctcagcaacagagcagaagctccatctcaaaaaaaaaaaaaa 2033			
Db	375 CACCACTGCACATCCAGCCTGGGCAACAGAGTGAAGTGGTCTCTTAATAATAATAATAA 434			
QY	2034 aaagaagaaaaaga 2048			
Db	435 TAAATATAATAATGA 449			
RESULT 10				
AM970571				
LOCUS	AM970571	521 bp	mrna	linear
DEFINITION	EST382652 MAGE resequences, MAGK Homo sapiens cDNA, mRNA sequence.			
ACCESSION	AM970571			
VERSION	AM970571.1	GI:8160416		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1 (bases 1 to 521)			
4	Hogde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt			

TITLE	I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.			
JOURNAL	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray			
COMMENT	Unpublished (2000) Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnq@tigr.org Plate: 279			
FEATURES	Seq primer: Forward. Location/Qualifiers			
SOURCE	1..521 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MAGE resequences, MAGK" /note="Vector: pBluescriptSM"			
BASE COUNT	162 a	128 c	141 g	89 t 1 others
ORIGIN				
Query Match	7.3%	Score 239.2,	DB 9,	Length 521;
Best Local Similarity	82.5%	Pred. No. 8,8e-25;		
Matches 274:	Conservative	0;	Mismatches 58;	Indels 0;
Gaps	0;			
QY 1723	aaaatcaagctgtgctggctggctggctgctcctataatcccgacaccttgggaagc	1782		
Db 167	AGAAATACCTTCGGCGCGGCGCACATGCTCATGCTGTAAATCCAGCATTTTGGGAGGC	226		
QY 1783	cgaagctggcgctatccctgaagctcagaagcttgtgacccagctggccaacatggtga	1842		
Db 227	CGAGCGGGGTGATCACTGAGCTCAGGAGTTCAGAGACACGAGCTCTCAACATGGCGA	286		
QY 1843	cccactttaccaaaataataaaattgacgggcattgtgtgctgacattgtatccc	1902		
Db 287	CCCCCTCTCTACTAAAAATACAAAAATTAGCCGGCGTGTGGCGCCCTGTAAATCTC	346		
QY 1903	agctacttgggaagctggagcaagaagaatcgcttgaacccagagagaagtgacgtg	1962		
Db 347	AGCAACTCGGGAGCGCTGAGCGAGGAATCACTTGAGCCCGAGAGCGACGCTTGCA	406		
QY 1963	agctgaagctcggtgcctgacactcagaactcagaacagagagagacatctcaaaa	2022		
Db 407	AGCCAGATTCGACACACTGCACCTCCAGCTGGGCGACAGAGGAGACCTCGCTCA	466		
QY 2023	aaaaaaaaaaaaaaaaaagaaaaaaga 2054			
Db 467	AAAAAAAAAAAAAAAAAGAAAAAAAAAAAAA 498			
RESULT 11				
AG156412/c				
LOCUS				
DEFINITION	AG156412 669 bp DNA linear GSS 09-JAN-2002			
ACCESSION	Pan troglodytes DNA, clone: RP43-021A10.TJ, genomic survey			
VERSION	AG156412			
KEYWORDS	AG156412.1 GI:16686090			
SOURCE	GSS; GSS (genome survey sequence).			
ORGANISM	Pan troglodytes male lymphocytes DNA, clone_1lb:RPCI-43 Chimpanzee			
REFERENCE	Male BAC Library clone:RP43-021A10.TJ.			
AUTHORS	Pan troglodytes			
TITLE	Eukaryotes: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.			
REFERENCE	1 (stiles)			
AUTHORS	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,			
TITLE	Totoki,Y., Watanabe,H. and Sakaki,Y.			
JOURNAL	BAC end sequences of Library RPCI-43			
REFERENCE	Unpublished			
AUTHORS	2 (bases 1 to 669)			
	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,			
	Totoki,Y., Watanabe,H. and Sakaki,Y.			

JOURNAL
MEDLINE
COMMENT

scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallaceu.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.hsc.washington.edu>
Plate: 2277 row: M column: 20

Seq primer: T7
Class: BAC ends
High quality sequence stop: 897.

location/Qualifiers

1. 897

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2277 Col=20 Row=M"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: Sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

Query Match	7.3%	Score 239.2	DB 12	Length 897
Best Local Similarity	83.4%	Pred. No. 7e-25		
Matches 271	Conservative 0	Mismatches 54	Indels 0	Gaps 0
OY 1723	aaaatcagagcttgctgcgtgcgctggtcctatgcttaataatccacagacttggagac	1782		
Db 268	AATCAGAAAGGCTCTGGTTGGGGCGGTGGCTCACACTGTAAATCCACGACTTTGGGAAGC	327		
OY 1783	cgagatggcgctatccctctgagctgacgaagattgtgacacagcttggccaacatggtgaa	1842		
Db 328	CGAGTTGGGTGGATGCACCTTAAGTCAAGGAATTTGGGACACAGCCTGGCCAACTGCGCAAA	387		
OY 1843	ccccatctttacccaaaaataaaataagccgggacatggtggctgtgactgtatccc	1902		
Db 388	CCCCATCTCTCTATAAAATACAAAAATTAGCCGGGCAACGTGGCGGCACTGTATATCCC	447		
OY 1903	agccactctgggaagccttgaggaagaagatcgcttaaccacgaagacggaatggcagt	1962		
Db 448	AGCTACTTGGAAAGGCTGAGGCAAGAGATTCGTTAAACCCGGGAGGCAAGAAATTTCAGAG	507		
OY 1963	agcttgaagatcgctgcgctgtgacactccagcctcagcacagacgagagactccatcaaaa	2022		
Db 508	AGCTGAGATTTGTGCCCGCTGCACCTCCAGCCTGNGTGACAGAGTGAACATTCATTTATAA	567		
OY 2023	aaaaaaaaaaaaaaaaaaaaaaag	2047		
Db 568	TAAATTAATTAATTAATATTATTAAG	592		
RESULT 13				
AM020150				
LOCUS				
DEFINITION	AM020150	397 bp	mRNA	linear
IMAGE:2482456 5', mRNA sequence.				
ACCESSION	AM020150			
VERSION	AM020150.1	GI:5873680		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	homo sapiens			
REFERENCE	Mumayyoti: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R. and Morton, C.C.			

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 27, 2002, 12:29:18 ; Search time 91.27 Seconds
(without alignments)
8873.164 Million cell updates/sec

Title: US-09-476-202a-1

Perfect score: 3297
Sequence: 1 ttaatcatggaatttca.....gtaagcaacccgccacca 3297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCrus.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	241.2	7.3	2499	1 US-08-485-618-96	Sequence 96, Appl
2	241.2	7.3	2499	1 US-08-605-672-96	Sequence 96, Appl
3	241.2	7.3	2499	2 US-08-482-293A-96	Sequence 96, Appl
4	241.2	7.3	2499	2 US-08-943-363-96	Sequence 96, Appl
5	241.2	7.3	2499	2 US-09-193-043-96	Sequence 96, Appl
6	241.2	7.3	3726	1 US-08-173-497-1	Sequence 1, Appl
7	241.2	7.3	3726	1 US-08-286-889-1	Sequence 1, Appl
8	241.2	7.3	3726	1 US-08-485-618-1	Sequence 1, Appl
9	241.2	7.3	3726	1 US-08-362-652-1	Sequence 1, Appl
10	241.2	7.3	3726	1 US-08-605-672-1	Sequence 1, Appl
11	241.2	7.3	3726	2 US-08-482-293A-1	Sequence 1, Appl
12	241.2	7.3	3726	2 US-08-943-363-1	Sequence 1, Appl
13	241.2	7.3	3726	1 US-09-193-043-1	Sequence 1, Appl
14	241.2	7.3	3785	1 US-08-485-618-98	Sequence 98, Appl
15	241.2	7.3	3785	1 US-08-605-672-98	Sequence 98, Appl
16	241.2	7.3	3785	2 US-08-482-293A-98	Sequence 98, Appl
17	241.2	7.3	3785	2 US-08-943-363-98	Sequence 98, Appl
18	241.2	7.3	3785	4 US-09-193-043-98	Sequence 98, Appl
19	241.2	7.3	3956	1 US-08-485-618-97	Sequence 97, Appl
20	241.2	7.3	3956	1 US-08-605-672-97	Sequence 97, Appl
21	241.2	7.3	3956	2 US-08-482-293A-97	Sequence 97, Appl
22	241.2	7.3	3956	2 US-08-943-363-97	Sequence 97, Appl
23	241.2	7.3	3956	4 US-09-193-043-97	Sequence 97, Appl
24	236.2	7.2	22481	4 US-08-367-841A-43	Sequence 43, Appl
25	236.2	7.2	22481	5 PCT-US95-07201-43	Sequence 43, Appl
26	234.4	7.1	17327	1 US-07-906-871-15	Sequence 15, Appl
27	233.2	7.1	36741	4 US-09-301-665-3	Sequence 3, Appl

28	231.8	7.0	2115	1 US-08-395-800A-7	Sequence 7, Appl
29	230.8	7.0	9365	4 US-09-608-285A-8	Sequence 8, Appl
30	230.8	7.0	14747	4 US-09-608-285A-42	Sequence 42, Appl
31	230.8	7.0	15977	4 US-09-608-285A-59	Sequence 59, Appl
32	230.6	7.0	8453	4 US-09-167-661-45	Sequence 45, Appl
33	229.6	7.0	841	5 PCT-US93-06251-80	Sequence 80, Appl
34	229.6	7.0	841	5 PCT-US93-06251-81	Sequence 81, Appl
35	229.6	7.0	3627	4 US-09-323-873A-6	Sequence 6, Appl
36	228.4	6.9	619	4 US-09-385-982-358	Sequence 358, App
37	228.2	6.9	1701	4 US-09-078-294-9	Sequence 9, Appl
38	228.2	6.9	4823	2 US-08-457-254-5	Sequence 5, Appl
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40	228.2	6.9	4823	3 US-08-999-927-5	Sequence 5, Appl
41	228.2	6.9	4823	4 US-08-461-819-5	Sequence 5, Appl
42	228.2	6.9	4823	5 PCT-US94-08806-28	Sequence 28, Appl
43	228.2	6.9	4823	5 PCT-US95-01829-5	Sequence 5, Appl
44	228.2	6.9	4823	5 PCT-US95-16626-5	Sequence 5, Appl
45	227.8	6.9	3867	4 US-09-347-114A-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-08-485-618-96
Sequence 96, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: Van der Vieren, Monica
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 2499 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-485-618-96

Query Match	7.38;	Score 241.2;	DB 1;	Length 2499;
Best Local Similarity	72.68;	Pred. No. 2.7e-44;		
Matches 411; Conservative	0;	Mismatches 13;	Indels 142;	Gaps 2

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QY	2773	ctggggagaaactaactacaagaaggttctcctctcctctctctgagctctcgagctcgagagatcat	283
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QY	2833	ccagaacagttcccgagcgccagcccaagtagttccctctgcaagagctcgagagaggggtgtg	289
Db	402	ccaagacagttcccccacgcccacgc-----	424
QY	2893	ggcccccgagtgatcttcgatctctctcccatctcccccacagatggtccaacaagaag	295
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QY	2953	atgagacatcgctctcctcgtatctgacggtcctctgaaagcatctgacccaagaatgacttaacag	301
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QY	3013	atgaaagggctctgtccaaagctgtcatatgagctgggcagtttgaaaggaactgacacccctgtgaag	307
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QY	3073	actggygaacaaatagtaaacaggaagcaactgagccctctggccctccccaactgacctgtgcagt	313
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QY	3133	ctgcaactgactgactactcaaacctcctctgaagatccaacttcaactcaccacatccgga	319
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QY	3193	ccagcccgagccagcagaagcctctgtgattccaactgttccaactgaaagagcctgacgttca	325
Db	620	ccagcccgagccagcagaagcctctgtgattccaactgttccaactgaaagagcctgacgttca	679
QY	3253	cgagccagggcactctgaagctgtgtg	3278
Db	680	cgagccagggcactctgaagctgtgtg	705

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1  APPLICATION NUMBER:  US 08/173,497
2  FILING DATE:  23-DEC-1993
3  PRIOR APPLICATION DATA:
4  APPLICATION NUMBER:  US 08/286,889
5  FILING DATE:  5-AUG-1994
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER:  US 08/362,652
8  FILING DATE:  21-DEC-1994
9  ATTORNEY/AGENT INFORMATION:
10 NAME:  Williams Jr., Joseph A.
11 REGISTRATION NUMBER:  38,659
12 REFERENCE/DOCKET NUMBER:  27866/32684
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE:  312-474-6300
15 TELEFAX:  312-474-0448
16 TELEX:  25-3856
17 INFORMATION FOR SEQ ID NO:  96:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH:  2499 base pairs
20 TYPE:  nucleic acid
21 STRANDEDNESS:  single
22 TOPOLOGY:  linear
23 MOLECULE TYPE:  DNA
24 US-08-605-672-96

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Query Match	7.3%;	Score 241.2;	DB 1;	Length 2499;
Best Local Similarity	72.6%;	Pred. No. 2.7e-44;		
Matches 411; Conservative	0;	Mismatches 13;	Indels 142;	Gaps 2

QY	2713	gysactctcgtactcaagaagcttcgtccctccaaagcgtctgtgcccgaacctgtcaagaagctctg	277
Db	282	GGCAGCTCCACCAACGGCTCCCGGGCTCCGGGCTGTGGCCACACCTGTGACAGACTCTGG	341
QY	2773	tgg9gagaactacataccccaagaagttccgtgcctccctgtgtggtctcgctg9gagatacat	283
Db	342	TGGGGAAACTCATACCTCAAGGTTCTCTCCTCTCTGTGGGTCCCGCTGGGAGATCTAT	401
QY	2833	ccagaacgtcccccgaagccgaagcgaagtgaagtcctctgcaagaagctgcagaag9g9ggttg	289
Db	402	CCAGACAGTCCCGACGCCACAGC-----	424
QY	2893	ggcccccgaaagtgcatactccgattcctcccatcccccacagagtgctcaatacaaga9	295
Db	425	-----CAAGTGTCCACATCAAGAG	444
QY	2953	atggacaatcgtctctcgtatctgacggtcgtcgtgaagcatgacccaagaatgacttaacag	301
Db	445	ATGGACATCTGTCTTCGTGATTGAAGGCTGTGGAAGATTTGACCAAAATGACTTTTAAACAG	504
QY	3013	atgaagagctcttgccaagctgtcatatggtgcagtttgaaaggcaatgcacacctgtgtgaag	307
Db	505	ATGAAAGGGCTTTTCCAAAGCTGTCAATGGGGCAATTGTAGGGGCACTGACACACCT-----	557
QY	3073	actggygaacaacatagtaaacagcactgagcccttggccctcccaactgtgccttggagt	313
Db	558	-----GT	559
QY	3133	ttagcactgatalgcagtaactcaaacctccttgaagaatccacttcaactcaccatccoga	319
Db	560	TTGCACATGATGACGATGACTCAAACTCCTGTGAAGATTCACCTTCACTTCAACCAATTCGGA	619
QY	3193	ccagcccgagccagcagcagagcgtgtgtgatatcccatcgttccaaactgaaagcctgtacgttca	325
Db	620	CCAGCCCGAGCCAGCAGAGACCTGTGTGAATCCCATGTCACATGAAAGGCGTACGTCTCA	679
QY	3253	cggccacggcgcatcctgcacagtggtg	3278
Db	680	CGGCCACGGGCAATCTTGACAGTGGTG	705

RESULT 3
US-08-482-293A-96

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: Sequence 96, Application US/08482293A
: Patent No. 5831029
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: GENERAL INFORMATION:
: APPLICANT: Gallatin, W. Michael
: APPLICANT: Van der Vleren, Monica
: TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
: NUMBER OF SEQUENCES: 103
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 233 South Wacker Drive, 6300 Sear Tower
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/482,293A
: FILING DATE:
:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/173,497
: FILING DATE: 23-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/286,889
: FILING DATE: 5-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/362,652
: FILING DATE: 21-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams Jr., Joseph A.
: REGISTRATION NUMBER: 38,659
: REFERENCE/DOCKET NUMBER: 27866/32684
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
:
: TELEX: 25-3856
:
: INFORMATION FOR SEQ ID NO: 96:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2499 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
:
: US-08-482-293A-96

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	Query Match	7.3%	Score 241.2;	DB 2:	Length 2499;
	Best Local Similarity	72.6%;	Pred No. 2.7e-44;		
	Matches 411; Conservative	0;	Mismatches 13;	Indels 142;	Gaps
Oy	2713 ggaacctggtccacaggtcttgcctccaagcgtgtgcccagacctgacagaagtctg	2772Z			
Db	282 GGCACGCTCCACCACCAAGGGCTCCCGGTCTTGCTGTGGCTTGGCCCCGACCTTCACAGATGCTGG	341			
Oy	2773 tggggaactcatctactcaaaaggatttcctgcgtccctgcgtcggtcgctgcgttggaatat	2832Z			
Db	342 TGGGGAAACTCATCTACTCAAAGGGTTCTGCTCCTCGCTGCGTGGGCTGGGGAATATAT	401			
Oy	2833 ccagacagtcgcccgacgacgaccagtagtcttcctgycagagctgcagaagaaggggttg	2892Z			
Db	402 CCAACACAGTCCCAGCACGCCACGC-----	424			
Oy	2893 ggcccccgagtgatcttcgatcttcctcccatctcccccacagatgtcccatcaag	2952Z			
Db	425 -----CAGAGTGTCCATATAAAG	444			
Oy	2953 atggacaatcgtctctctcgtatgcagcgtctggaagcatgtaccaaatgaacttaaccag	3012Z			
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OY	3193	ccagcccgagccagcagagagcctgtgtgataccatgctccaactgaaagcgctgaagttca	3253
Db	620	CCACCCCGAGCCAGCAGAGCGCTGTGGATCCCATCGTCCACTGAAAGGCGTAGAGCTTCA	679
OY	3253	cgagccgggacatccctgaacagtgtg	3278
Db	680	CGGCGACGGGCACTCTACAGTGGTG	705

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US-08-943-363-96          RESULT      4
US-08-943-363-96          US-08-943-363-96
: Sequence 96, Application US/08943363
: Patent No. 5837478
: GENERAL INFORMATION:
: APPLICANT: Gallatin, W. Michael
: APPLICANT: Van der Vieren, Monica
: TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
: NUMBER OF SEQUENCES: 114
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 233 South Wacker Drive, 6300 Sear Tower
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/943,363
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/173,497
: FILING DATE: 23-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/286,889
: FILING DATE: 5-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/362,652
: FILING DATE: 21-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams Jr., Joseph A.
: REGISTRATION NUMBER: 38,659
: REFERENCE/DOCKET NUMBER: 27866/32684
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 96:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2499 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: US-08-943-363-96

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Query Match 7.3%, Score 241.2; DB 2; Length 2499;
Best Local Similarity 72.6%; Pred. No. 2.7e-44;
Matches 411; Conservative 0; Mismatches 13; Indels 142; Gaps 2;

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QY 2893 ggcccccgagctgacatcccgatccctccatcccccacagagctgcacatcaagag 2952
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RESULT 5
US-09-193-043-96
; Sequence 96, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 2499
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-193-043-96

Query Match 7.3%, Score 241.2; DB 4; Length 2499;
Best Local Similarity 72.6%; Pred. No. 2.7e-44;
Matches 411; Conservative 0; Mismatches 13; Indels 142; Gaps 2;

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QY 2773 tgggagagacacacacacacacacacacacacacacacacacacacacacacacacacac 2832
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QY 3073 actgggacaacaatagtaacagcagcagcagcagcagcagcagcagcagcagcagcagc 3132
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Db 558 -----gt 559
QY 3133 ttgacatgattgacagtaactcaaacctctgaagatcacaacttaaccattcaaccattccgga 3192
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Db 560 ttgacatgattgacagtaactcaaacctctgaagatcacaacttaaccattcaaccattccgga 619
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Db 620 ccagcccgagccagcagagcctgtgtgacccatcgctccaactgaagaagcctgacgttca 679
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Db 680 cgagcagggcagcctctgacagtggtg 705
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RESULT 6
US-08-173-497-1
; Sequence 1, Application US/08173497
; Patent No. 5437958
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van Der Vlieten, Monica
; TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,497
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

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1 NAME: No. 5437958and,Greta E.
2 REGISTRATION NUMBER: 35,302
3 REFERENCE/DOCKET NUMBER: 27866/31363
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 312-474-6300
6 TELEFAX: 312-474-0448
7
8 TELEX: 25-3856
9
10 INFORMATION FOR SEQ ID NO: 1:
11
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 3726 base pairs
14 TYPE: nucleic acid
15 STRANDEDNESS: single
16 TOPOLOGY: linear
17 MOLECULE TYPE: cDNA
18 FEATURE:
19 NAME/KEY: CDS
20 LOCATION: 3..3485
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Query Match	7.3%	Score 241.2	DB 1	Length 3726
Best Local Similarity	72.6%	Pred. No. 3.1e-44		
Matches 411; Conservative	0;	Mismatches 13;	Indels 142;	Gaps 2

QY	2713	ggaactctggcttaacaggtcttgcgtcccaaggccgtgtggcccgaccctgcacaaggtcttg	2772
Db	281	GGCAGCCTCCACCAACAGCGCTCCGGCTCTGGCTGTGTGGCCGACCCCTGCACAGGTGTG	340
QY	2773	tggggagaaactcatactcaaaaggttcttcgtcctcctcgtcgtggtcgcgtcgtggaatcat	2832
Db	341	TGGGGAGAACTCATCTACTCAAAGGGTTCTGTGCTCGTGGGCTCGGGCTGTGGAGATCAT	400
QY	2833	ccagacagttcccccagcgccacgcccaggtagttccctbgcagaagctgcagaagggggttg	2892
Db	401	CCAAACAGTCCCGACGCCACGC-----	423
QY	2893	ggcccccgatgcattccgatctcctcccatctcccccacagagttgcacatcaag	2952
Db	424	-----CAGAGTGTCCACATCAAGAG	443
QY	2953	atgacatacgtctcttcctcgtatctgacggtctctggaagcatgacaacaaatgacttaacag	3012
Db	444	ATGACATCCTCTTCTTCGATTGACGGCTCTGGAGACATGACCAAAATGACTTTAACAG	503
QY	3013	atggaaggtcttctccaagctgtgtcattgagggccaggtttgaggagcactgcacacctggtgaag	3072
Db	504	ATGGAAGGGCTTTTCTCCAAAGCTGTCAAGGGGCCAGTTTGAAGGACATCAACACCT-----	556
QY	3073	actggygaacaataagtaacagacgtgagccctggyccctcccccacttgcgtcttgacgt	3132
Db	557	-----GT	558
QY	3133	tctgactgattgcagtaactcaaacctccttgaagaatcacttcaacttccaccatcgcga	3192
Db	559	TTGCACATGATGACGTACTCAAACTCTCTGAAGTCCACTTCACTTCAACCCCAATTCCGGA	618
QY	3193	ccagccccgagccagcagagagctgtgtgagatcccatcgttccaactgaagaagccttgacgttca	3252
Db	619	CCAGCCCGAGCCAGCAGAGAGCTGTGTGATGCCATCTCCAACTGAAAGCCCTGAGTGTCA	678
QY	3253	cgagccagggcatccttcgaacgtgtgtg	3278
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RESULT 7
 US-08-286-889-1
 : Sequence 1, Application US/08286889
 : Patent No. 5470953
 : GENERAL INFORMATION:
 : APPLICANT: Gallatin, W. Mich
 : APPLICANT: Van der Vieren, Monica
 : TITLE OF INVENTION: No. 5470953el Human 2 Interferin Alpha Subunit

```

NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3..3485
US-08-286-889-1

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Query Match	7.38;	Score 241.2;	DB 1;	Length 3726;
Best Local Similarity	72.68;	Pred. No. 3.1e-44;		
Matches 411; Conservative	0;	Mismatches 13;	Indels 142;	Gaps 2;

QY	2713	ggactcttgctcaagagctcttgctctccaagcgtcttgcccgaccctgcacaaagtctg	2772
Db	281	GGGACGCTCCACCAACGGCTCCCGGGTCTCGGCTCTTGCCCGACCCCTGCACAGATGTCG	340
QY	2773	tggaggaactacatcacaaaggtcttcgtccctcgtcgtcggctcgcgtctggaaatcat	2832
Db	341	TGGGGAGACTCATACTCAAAAGGCTCTGCTCCCTGCTGGGCTGGCGCTGGGAATCAT	400
QY	2833	ccagacagctcccgacgcacacgcgaagtgaagtcctctgcagagagctgcagaagagggttg	2892
Db	401	CCAGACAGTCCCGGACGCCACGC-----	423
QY	2893	ggcccccgagtgatctccgatctctcccaatctccccaagatgtccaatatgaag	2952
Db	424	-----CAGATGTGTCACATCAATCAAG	443
QY	2953	atgacatactcttcctcgatctgaacggtcgtgcgaagcattgaccaaatgaacttaacag	3012
Db	444	ATGACATCTGCTTCTCTGATTGACGGCTCTGGAAAGCATTTGACCAAAATGACTTTAACCAG	503
QY	3013	atgaagagccttctgcacagctgtcatcgtgcagatttgaagagcactgcacacacctgtgtgaag	3072
Db	504	ATGAAGGGCTTTGTCCAAGCTGTCAATGGGCAATTGAGGGCAGTCGACACCCCT-----	556
QY	3073	actcggcaacaatatgaacaggcactgaagcccttggccctcccaacttggcctttgcagct	3132
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QY 3133 ttgacatgatgcagttactcaaaactctgaaagatccacttaacttaaccccaattccgga 3192
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 Db 559 TTGACATGATGCAGTACTCAAACTCTGGAAGATTCACCTTACCTTCAACCAATTCGGA 618
 QY 3193 ccagcccgagccagcagagccttgg tggatcccatcgctcccaactgaaagcctgacgttca 3252
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 Db 619 CCAGCCCGAGCCAGCAGAGCCTTGCTGATCCCATCGTCCAACTGAAGGCTTGACCTTCA 678
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RESULT 8

US-08-485-618-1
 ; Sequence 1, Application US/08485618
 ; Patent No. 5728533
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
 ; NUMBER OF SEQUENCES: 103
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive, 6300 Sear Tower
 ; City: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,618
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/173,497
 ; FILING DATE: 23-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/286,889
 ; FILING DATE: 5-AUG-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/362,652
 ; FILING DATE: 21-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Williams Jr., Joseph A.
 ; REGISTRATION NUMBER: 38,659
 ; REFERENCE/DOCKET NUMBER: 27866/32797
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ. ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3726 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 3..3485
 ; US-08-485-618-1

Query Match 7.3%; Score 241.2; DB 1; Length 3726;
 Best Local Similarity 72.6%; Pred. No. 3.1e-44;
 Matches 411; Conservative 0; Mismatches 13; Indels 142; Gaps 2;
 QY 2713 ggaactctggtccacagagcttctgctcctcagagcctgtggccgacccctgacagagtcgtg 2772

Db 281 GGCAGCCTTCACCAAGCGCTCCGGCTCTGGCCCTGTGGCCCGACCCCTGCACAGACTGTG 340
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 Db 341 TGGGAGAACTCATACTCAAAAGGTTCTGCTCTCTGCTGAGGCTGGGCTGGGATCAT 400
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 Db 401 CCAGACAGTCCCGACGACGACG----- 423
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 Db 444 ATGCACATCGCTTCTCGATTGAGCGGCTGTGGAAGCATTTGACAAATGACTTTAACGAG 503
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RESULT 9

US-08-362-652-1
 ; Sequence 1, Application US/08362652
 ; Patent No. 5766850
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
 ; NUMBER OF SEQUENCES: 93
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive, 6300 Sear Tower
 ; City: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/362,652
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/173,497
 ; FILING DATE: 23-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/286,889
 ; FILING DATE: 5-AUG-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Williams Jr., Joseph A.


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; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; NAME/KEY: CDS
; LOCATION: 3..3485
; US-08-362-652-1

Query Match      7.3%; Score 241.2; DB 1; Length 3726;
Best Local Similarity 72.6%; Pred. No. 3.1e-44;
Matches 411; Conservative 0; Mismatches 13; Indels 142; Gaps 2;

QY 2713 ggaactcgtgtcacaggcttcctgcctccagcgtgtgtgcccgaacctgtgcagaatctg 2772
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RESULT 10
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; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,672
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..3485
; US-08-605-672-1

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Best Local Similarity 72.6%; Pred. No. 3.1e-44;
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 ; APPLICANT: Van der Vlieten, Monica
 ; TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
 ; NUMBER OF SEQUENCES: 103
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive, 6300 Sear Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
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 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/173,497
 ; FILING DATE: 23-DEC-1993
 ; PRIOR APPLICATION DATA:
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 ; FILING DATE: 5-AUG-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/362,652
 ; FILING DATE: 21-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Williams Jr., Joseph A.
 ; REGISTRATION NUMBER: 38,659
 ; REFERENCE/DOCKET NUMBER: 27866/32684
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3726 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 3..3485
 ; US-08-482-293A-1

Query Match 7.3%; Score 241.2; DB 2; Length 3726;
 Best Local Similarity 72.6%; Pred. No. 3.1e-44;
 Matches 411; Conservative 0; Mismatches 13; Indels 142; Gaps 2;

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 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Van der Vlieten, Monica
 ; TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
 ; NUMBER OF SEQUENCES: 114
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive, 6300 Sear Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/943,363
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/173,497
 ; FILING DATE: 23-DEC-1993

LENGTH: 3785 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3486
US-08-605-672-98

Query Match 7.3%; Score 241.2; DB 1; Length 3785;
Best Local Similarity 72.6%; Pred. No. 3.1e-44;

Matches 411; Conservative 0; Mismatches 13; Indels 142; Gaps 2;

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XX	07-NOV-2001	
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XX	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36910.	
KW	Cytostatic; gene therapy; vaccine; metastasis; ds.	
XX	Cytostatic; gene therapy; vaccine; metastasis; ds.	
OS	Homo sapiens.	
XX	Homo sapiens.	
PN	WO200157182-A2.	
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PR	20-OCT-2000	2000US-0241808.
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PR	01-NOV-2000	2000US-0244617.
PR	08-NOV-2000	2000US-0246474.
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PR	08-NOV-2000	2000US-0246476.
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PR	08-NOV-2000	2000US-0246523.
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PR	17-NOV-2000	2000US-0249212.
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PR	17-NOV-2000	2000US-0249244.
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PR	17-NOV-2000	2000US-0249264.
PR	17-NOV-2000	2000US-0249265.
PR	17-NOV-2000	2000US-0249297.
PR	17-NOV-2000	2000US-0249299.
PR	17-NOV-2000	2000US-0249300.
PR	01-DEC-2000	2000US-0250160.
PR	01-DEC-2000	2000US-0250391.
PR	05-DEC-2000	2000US-0251030.
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PR	08-DEC-2000	2000US-0251869.
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PR	11-DEC-2000	2000US-0254907.
PR	05-JAN-2001	2001US-0259678.
PA	(HUMA -) HUMAN GENOME SCI INC.	
PI	Rosen CA, Barash SC, Ruben SW:	
PI	WPI: 2001-483426/52.	
DR		
XX		
PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating cancers and	
PT	metastasis -	
XX		
PS	Disclosure; SEQ ID NO 36910; 3071pp + Sequence Listing; English.	
XX		
CC	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)	
CC	amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic	
CC	activity, and can be used in gene therapy and vaccine production. (I)	
CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
CC	treatment of diseases associated with inappropriate (I) expression. For	
CC	example, they may be used to treat disorders associated with decreased	
CC	expression by rectifying mutations or deletions in a patient's genome	
CC	that affect the activity of (I) by expressing inactive proteins or to	

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 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
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 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-483426/52.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Disclosure: SEQ ID NO 24134; 3071pp + Sequence Listing: English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytosolic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome

CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 51469 BP; 13004 A; 12589 C; 13305 G; 12571 T; 0 other;
 Query Match 7.5%; Score 247; DB 22; Length 51469;
 Best Local Similarity 80.5%; Pred. No. 3.7e-39;
 Matches 289; Conservative 0; Mismatches 70; Indels 0; Gaps 10;
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 DB 28714 GCAACACAGTAAGACCCCATCTCTAAATAATATGCGCGGCGCAGTGTCTAT 28655
 QY 1756 gcttatatcccgacattggagagcgagatgagtgatccctcaggtcaggaatt 1815
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 QY 1816 gtgaccagcctggccaacatggtgaaccccatcttaccacaaataataaattacgcg 1875
 DB 28594 GAGACGAGCCTGGCCACATGCTGAATCCCACTACCTACCTGAGGAGGAGCAATCGCT 28535
 QY 1876 ggcatgtgtgcgtgcaactgtaatccagctacttgggaagctgaggaagaatcgct 1935
 DB 28534 GGCATGCTGGCATGACACTCTAATCCAGCTACTCGGAGGCTGAGGACGAGAAATCGCT 28475
 QY 1936 tgaacccagagagcaggaagttgagtgatgagtgctgctgctgacccagcctcag 1995
 DB 28474 TGAACCCGAGGAGGAGGCTGTAGTGAGCCGAGATCATCCACTGCACCTCAGCTGGG 28415
 QY 1996 caacagagcagagactccatctcaaaaaaataaaaaaataaaaaaaga 2054
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 AC AAK70270;
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 DT 06-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25082.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KM cytosolic; gene therapy; vaccine; metastasis; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01354.
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 PR 31-JAN-2000; 2000US-0179065.
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PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
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PR 17-NOV-2000; 2000US-0249215.
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PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
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PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
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PR 08-DEC-2000; 2000US-0251889.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-02539678.

(HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
PI Rosen CA, Barash SC, Ruben SM:
XX WPI; 2001-483426/52.
XX
DR
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
PS
XX Disclosure; SEQ ID NO 25082; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM62170 to AAM91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased

CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK67694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 51469 BP; 13004 A; 12589 C; 13305 G; 12571 T; 0 other;

Query Match 7.5%; Score 247; DB 22; Length 51469;
Best Local Similarity 80.5%; Pred. No. 3.7e-39;
Matches 289; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1696 gcatatagatcattcattcgtgcaatcaaaatcaggcttggctggtgctggtgctcat 1755
DB 28714 GCNACACAGTAAGACCCCATCTCTAATAAATATATATGCGCGGCGAGTGCAT 28655
QY 1756 gcttataatccagacttggagagcgagatggcgatcccttgaggtcaggaattt 1815
DB 28654 GCGTGCATATCCACGACACTTTGGAGGCCGAGGTAGGAGGATCACCCTGAGTCAAGAGTTT 28595
QY 1816 gtgacagccttggccacatgttgaaccccatcttaccacaaatataaataatgacg 1875
DB 28594 GAGACACAGCTGGCCCAACATGCTGAACCCCACTCTAATAAATATATTAATGTTG 28555
QY 1876 ggcattggtgggtgacttgaatcccgacttcttggagagctgaggaagaatcgct 1935
DB 28534 GGCATGTGTGATCCTCTGTAATCCACGCTACTCGGAGAGCTGAGCGAGAGATCGCT 28475
QY 1936 tgaacccagagagagagagagtgctgagctgagctgctgctgctgctgctgctg 1995
DB 28474 TGAACCCGAGGAGGAGGAGGCTGTAGTGAGCCGAGATCATGCTGCTGCTGCTGCTG 28415
QY 1996 caaagagcgagagctcattcctcaaaaaaagaaaaaagaaaaaagaaaaaagaa 2054
DB 28414 TGATAGAGGAGAGACTGTCTCAATAATTAATAATTAATAATTAATAATTAATA 28356

RESULT 4
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ID AAK78813 standard; DNA; 51469 BP.
XX
AC AAK78813;
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DT 07-NOV-2001 (first entry)
XX

DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:33625.
XX

KW Human; Immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
XX cytostatic; gene therapy; vaccine; metastasis; ds.

OS Homo sapiens.
XX

PN WO200157182-A2.
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PD 09-AUG-2001.
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PF 17-JAN-2001; 2001WO-US01354.
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PR 31-JAN-2000; 2000US-0179065.
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PR 20-OCT-2000; 2000US-0241221.

CC	20-OCT-2000;	2000US-0241785.
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PR	20-OCT-2000;	2000US-0241787.
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PR	08-NOV-2000;	2000US-0246475.
PR	08-NOV-2000;	2000US-0246476.
PR	08-NOV-2000;	2000US-0246477.
PR	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246523.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246525.
PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246527.
PR	08-NOV-2000;	2000US-0246528.
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PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	08-NOV-2000;	2000US-0246613.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
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PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
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PR	17-NOV-2000;	2000US-0249216.
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PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249244.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
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PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251889.
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PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX		
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI; 2001-483426/52.	
XX		
XX		
PI	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PI	useful for preventing, diagnosing and/or treating cancers and	
XX	metastasis -	
PS	Disclosure; SEQ ID NO 33625; 3071bp + Sequence Listing; English.	
XX		
CC	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)	
CC	antio acid sequences given in AAK62170 to AAK91921. (I) have cytostatic	
CC	activity, and can be used in gene therapy and vaccine production. (I)	
CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
CC	treatment of diseases associated with inappropriate (I) expression. For	

CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AA654703
CC to AA87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AA54942 to AA634950 and AA882169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 51469 BP; 13004 A; 12589 C; 13305 G; 12571 T; 0 other;

	Query Match	Similarity	7.5%	Score 247;	DB 22;	Length 51469;
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Qy	1696	gcatacagatccatcatcaagctgcatcaaaatacagagcttgctggtgcggtgctcat	1755			
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Qy	1756	gcttataatcccacgaacelltgggaagccgagatlyggcgatatacccttgagtcagaattt	1815			
Db	28654	GCGTCGAATCCACGACACTTTGGGAGGCCACGAGTAGAGCATCACTGAGAGTGAAGGTTCC	28595			
Qy	1816	gtgaccagagcttgcccaaatgtgtgaataccccaactcttaccaaaataataaattagccg	1875			
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Qy	1876	ggcatgtgtgctgtgcacttgttaatcccgactacttgggaagcttgagcgaagaatcgct	1935			
Db	28534	GCGATGGTGGCATGCGACTGTAAATCCCACTACTCGGGAGGCGTGAAGGCAAGATCGCT	28475			
Qy	1936	ttaacccaggaagaacggaattgacgtgagcttagatcgctgcgctgacacacagcctcag	1995			
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Qy	1996	caacagagcagagactccatccatcacaataaaaaaaagaaagaaagaaagaaagaa	2054			
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ID	AA05811	standard; DNA; 3172 BP.				
XX						
AC	AA05811;					
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DT	21-NOV-2001	(first entry)				
XX						
DE		Human reproductive system related antigen DNA SEQ ID NO: 8499.				
XX						
KW		Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.				
OS		Homo sapiens.				
XX						
PN	WO200155320-A2.					
XX						
PD	02-AUG-2001.					
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FE	17-JAN-2001;	2001WO-US01339.				
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PR	31-JAN-2000;	2000US-0179065.				
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PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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PR 12-SEP-2000; 2000US-0231968.
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PR 20-OCT-2000; 2000US-0241221.
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PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
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PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
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PR 06-DEC-2000; 2000US-0251856.
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PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-02559678.
(HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition -
XX
XX
PS Disclosure; SEQ ID NO 8499; 1297pp + Sequence Listing; English.
XX
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.

PR 08-NOV-2000; 2000US-0246478.
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 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 03-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0251719.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMAN-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 PI
 DR WPI; 2001-483426/52.
 XX
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Disclosure: SEQ ID NO 40088; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169

CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 3172 BP; 908 A; 711 C; 529 G; 1024 T; 0 other;
 Query Match 7.58; Score 246; DB 22; Length 3172;
 Best Local Similarity 81.4%; Pred. No. 3.7e-39;
 Matches 285; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
 QY 1705 tcacatcacgtgcacccaataacacagctggtggtgcggtgctatgctataat 1764
 Db 971 TTTAAACCCCTTTAAAAAAGAGAGAGGCTGGGTGGGTCTCAGCCTATTAAT 912
 QY 1765 cccagcaatttggagggccgagatggtgcgtatccctcgaagtcagagattgtaccagc 1824
 Db 911 CCCAGCACTTTGGGAGGACAGGACGAGCAGATCACTCGAGGTGAGGATCAAGACAGC 852
 QY 1825 ctggccacaatgttgaaccccatccttaccaaaataataaattagccggagatgtg 1884
 Db 851 CTGGCCAAACATGGTGAACCCCATCTCTACTAAAAATATGATGGCGGTGTG 792
 QY 1885 gcgtgcacttgtaatcccaacttcttggaagctggaagcgaagaatcgcttgaaccag 1944
 Db 791 GTGGGTAACCTTAATCCCACTCTTGGAGGCTGAGGACGAGAAATCTTGAACCTTG 732
 QY 1945 gagacggaagttgcagtgatgagatgcgttgcgttgcactccagcctcagcaacagagc 2004
 Db 731 GAGGAGAGAGATTGGCAGTGAGCTGATCATGCCCTACTCTCCAGACTGATGACAGAGT 672
 QY 2005 gagatcccatctcaaaaaaaaaaaaaaaaaaagaagaagaagaaga 2054
 Db 671 GAGACTCATCTCAAAAAAAAAAAAAAAAAAATGAAATATAAAAA 622
 RESULT 7
 AAS28363/C
 ID AAS28363 standard; DNA; 32146 BP.
 XX
 AC AAS28363;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Genomic sequence #203 encoding for novel human respiratory antigen.
 XX
 KW Human; respiratory antigen; respiratory disorder; throat disorder;
 KW lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;
 KW anti allergic; anti asthmatic; anti inflammatory; olfactory;
 XX
 OS Homo sapiens.
 XX
 PN WO200155448-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01333.
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 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205115.
 PR 07-JUN-2000; 2000US-0209467.
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 PR 30-JUN-2000; 2000US-0215135.
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PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-476224/51.
XX
XX
PT Isolated polypeptide for treating, preventing and/ or prognosing
PT disorders related to the respiratory system including respiratory
PT cancers and also for testing and detection e.g. diagnosis -
XX
XX
PS Disclosure; SED ID NO 797; 546pp; English.
XX
XX

The present invention relates to the isolation of novel human respiratory antigens (AA017685-AA017975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders (e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy.

AA028161-AA028764 represent genomic sequences encoding for novel human respiratory antigens.

Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 32146 BP; 8745 A; 6747 C; 7148 G; 9506 T; 0 other:

Query Match 7.4%; Score 245.4; DB 22; Length 32146;
Best Local Similarity 86.8%; Pred. No. 7e-39;
Matches 270; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1736 ggcctgggtggcggcgcgcgtatataatcccgcaacttgggagagcgagatggcgta 1795
DB 7416 GCGCGGGCGGGGCTGCTCACGCGCTATATCCACGACTTGAAGCGTGTGAGCGGGGTGA 7357
QY 1796 tcccccctgaggtcagaggttgtagccagcctggccaacatgctgaaacccatcttacc 1855
DB 7356 TCACCTGGAATTCAGAGATTGAGACCAAGCCTGGCCAAACATGGGAAACCCCATCTACT 7297
QY 1856 aaaaataataaaattgacgggcatggtggcgtgcaactgtaatccagctacttggaa 1915
DB 7296 AAAAAATACAAAGTTAGCCAGCGGTGTGGCGGACACTTAATCCAGCTACTTGGGAC 7237
QY 1916 gctgagggcgaagaatcgccttgtaaacccagagacggaagttgagtgagctgagatcgtg 1975
DB 7236 GCTGAGGCGAGAGAAATGCTTGAACCGGAGAGAGGTGCGAGTGAAGCTGATCGTA 7177
QY 1976 ccgttcacatccagcctcagcaacagacgagactcctcatcctcaaaaaaataaaaaa 2035
DB 7176 CCACCTGCATCCGAGCCTGGGCAACAGAGCAAGACTCTTCTCAAGAAAAAATAAAAAA 7117
QY 2036 aagaaaaaataa 2046
DB 7116 CCCAAAAAAA 7106

RESULT 8

AAS36168
ID AAS36168 standard; DNA; 10434 BP.

XX AAS36168;

DT 17-DEC-2001 (first entry)

XX Human cardiovascular system antigen genomic DNA SEQ ID No 1668.

KW Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog;
KW antirheumatic; antiproliferative; cytosolic; cardiant; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; vitucide; fungicide; cancer;
KW ophthalmological; vitreary; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;
KW wound healing; skin aging; organ transplantation; tissue regeneration;
KW anti-fertility.

XX Homo sapiens.

XX WO200155321-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01340.

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
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PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
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PR 26-JUL-2000; 2000US-0220963.
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PR 17-NOV-2000; 2000US-0249300.
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PR 01-DEC-2000; 2000US-0250391.
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PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Disclosure; SEQ ID NO 34510; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)

CC amino acid sequences given in AAM82170 to AAM91921. (1) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (1)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (1) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (1) by expressing inactive proteins or to
CC supplement the patient's own production of (1). Additionally, (1)
CC polynucleotides may be used to produce the secreted (1), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (1) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.

XX Sequence 6154 BP; 1629 A; 1274 C; 1369 G; 1382 T; 500 other;

Query Match 7.4%; Score 244.8; DB 22; Length 6154;

Best Local Similarity 39.5%; Pred. No. 7.1e-39; Mismatches 1068; Indels 75; Gaps 9;

Matches 747; Conservative 1; Mismatches 1068; Indels 75; Gaps 9;

QY 142 ggcgtgagatggtgctcagcgcctgtatccagtaactttggagagagaggttggagga 201
DB 866 ggcgtggttcgtgtgctcagcgcctgtatccagtaactttggagagagaggttggagga 925

QY 202 ttgcttgatcagagagcctcagagcagatgagcaactatgagcgtatccttcttaca 261
DB 926 tcacttgagagcagaggttccagagccttgcagcaactatgagcaacttcttctact 985

QY 262 aaaaacaaaataatgagctgagcatgtgtgtcacaagtaaccagtgatc-ggag 320
DB 986 aaaaatacaaaaattagctgcggggtgtgtgtgcgcgcctgtatccagctatccggag 1045

QY 321 gctgaggtggaggaattgcttgagcttggaatttgaagctgcagtgagccctgatcatg 380
DB 1046 gctgaggtggaggaattgcttgagcttggaatttgaagctgcagtgagccctgatcatg 380

QY 381 ccacttcattccagcagctggcgacatagcaaaaactgtcaaaaaaaaagtctcc 440
DB 1106 ccacttcattccagcagctggcgacatagcaaaaactgtcaaaaaaaaagtctcc 440

QY 441 tctgcccacatagacaacacactctctgattctatctctgtagatgaatttgcaca 500
DB 1166 gctcagtgagggagacccctccagcagcagagcgtgtagagtagcagcagtagggaggt 1225

QY 501 tctcttgatataagaagaacacacatt-aggcattctgtgtctgtcttccact 559
DB 1226 gggaaaaatgagaccaaagatgatacacttctgcccctcccaacagatattctgtgt 1285

QY 560 taagataaattgaggttaaccgttatgttgcagaaactgcagctgtgtcttcttatt 619
DB 1286 gcaaccacattccctccctccctcccaatggaaggaaggggctgtg----- 1333

QY 620 tattgtaagaagaggtctgctgatagttgcctagagcttgctgcgaactgttgcctcaag 679
DB 1334 -----cgtrcaagccaacactcctcaagccggtcctgaa---gnaaccatag 1378

QY 680 caatccactgcgaagctcttggaacacagagcagtgacatgagcatctatc.ktgttlt 739
DB 1379 cctcccgctgttcggaatgagcctcactcaatttccaacaccttcttcttgaatacc 1438

QY 740 gatcttatctctgtgagtagtagccatgagcatgacttatatttgggtgtccatt 799
DB 1439 ttgttcccttctcattcaacaactcaagcctctcattcatgttgtt----- 1487

QY 800 ctctctggaggggtctgtcttttttgaacacacacccctgagctgagctctctccctg 859
DB 1488 -----ttttttttttagacaggtctgtctgtcaccagagcttgagag 1532

QY 860 cctctctgagcgtcaccacacatgccaagacctctgacgacattctgtcttcttct 919

DB 1533 -----gacgtgcacagatcaatggttcaactcagacttgacttctgtgacccaagcaat 1585

QY 920 tcaactccgttgagactagagagctaacggggtccctcggttaccacaactgtctctgag 979

DB 1586 ccttcgctcacaaccccccaggtagctgtgacgtgacgtacagggccacac-caccac 1644

QY 980 gcttgaggaggggtgtctctcttgaggaaaggaagccaagtlccctgcaggtttgtgaggg 1039

DB 1645 gcccgctaattttttttttttttttttttttttagagacagggctcagactatgtgmmmmnn 1704

QY 1040 gacagaatgaggttttccccaagatgtgtgtgcccctgcccaactctgttccata 1099

DB 1705 nnn 1764

QY 1100 ataaccaagccctcctactaccacactgtgcctccctcctcctgtgtgtgagggccctgac 1159

DB 1765 nnn 1824

QY 1160 atattttaactacccctctggaggttgagcactctgtgtctgtgttccccaacttcca 1219

DB 1825 nnn 1884

QY 1220 ctccctcaacgcgtctcaggtatgaccttcggcactgtgtcttctcgtagtgtata 1279

DB 1885 nnn 1944

QY 1280 gtggggcagaggtgtcgtgggagagcttggagaggttcgaagggtcctacatctggagag 1339

DB 1945 nnn 2004

QY 1340 gcaagcttgagggt 1399

DB 2005 nnn 2064

QY 1400 gctcattgtgcaggt 1459

DB 2065 nnn 2124

QY 1460 ggtcgtgtcaggt 1519

DB 2125 nnn 2184

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QY 1580 agtgagaggtccacagagccacagaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1639

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DB 2293 gctgaggt 2352

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QY 1760 atataccagcattgt 1819

DB 2413 gtaataccagcattgt 2472

QY 1820 ccagcttgagcagctgt 1879

DB 2473 ccagcttgagcagcagctgt 2532

QY 1880 tgggt 1939

DB 2533 tgggt 2592

QY 1940 ccagagagcagaggt 1999

Db 2593 cccggagagcagaggttgcaataagacaagatltgcatctgactccagctggcgac 2652
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Db 2653 agagcaagactcagtatcaaaaaaaaaa 2683

RESULT 10
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ID AAK82338 standard; DNA; 48908 BP.
XX
AC AAK82338;
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DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37150.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN W0200157182-A2.
PD
XX 09-AUG-2001.
PE 17-JAN-2001; 2001MO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
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PR 16-MAR-2000; 2000US-0189874.
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PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Disclosure; SEQ ID NO 37150; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
XX SO Sequence 48908 BP; 14764 A; 10631 C; 10740 G; 12773 T; 0 other;
Query Match 7.4%; Score 244.4; DB 22; Length 48908;
Best Local Similarity 84.4%; Pred. No. 1.2e-38;
Matches 275; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

DB 2496 tgaagcagatctcttgcacactccagccttggtgacagagcaagactccatccaa 2555
QY 2021 aaaaaaaaaaaaaaaaaaagaaaaaa 2046
DB 2556 aaaaaaaaaaagaaaaagaaaaa 2581
RESULT 11
AAK76168
ID AAK76168 standard; DNA: 25541 BP.
XX
XX AAK76168;
AC
AC
DT 07-NOV-2001 (first entry)
XX
XX Human immune/hematopoietic antigen genomic sequence SEQ ID NO:30980.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200157182-A2.
PN
XX
PD 09-AUG-2001.
XX
XX
XX 17-JAN-2001; 2001WO-US01354.
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XX
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PR 24-FEB-2000; 2000US-0184664.
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PR	05-JAN-2001	2000US-0254698

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM,
WPI; 2001-483426/52.

PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -

PS Disclosure; SEQ ID NO 30980; 3071pp + Sequence Listing; English.

CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients' own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK51942 to AAK54350 and AAK82169
CC represent sequences used in the exemplification of the present invention.

Query Match	7.4%;	Score 243.8;	DB 22;	length 25541;
Best Local Similarity	86.5%;	Pred. No. 1.4e-38;		
Matches 269;	Conservative 0;	Mismatches 42;	Indels 0;	Gaps 0;

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RESULT 12
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AC AAS28368;
XX
DT 07-NOV-2001 (first entry)
XX
DE Genomic sequence #208 encoding for novel human respiratory antigen.
XX
KW Human; respiratory antigen; respiratory disorder; throat disorder;
lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;
anti allergic; anti asthmatic; anti inflammatory; olfactory;
respiratory active; ds.
XX
OS Homo sapiens.
XX
PN WO20015448-A1.
XX
PD 02-AUG-2001.
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PF 17-JAN-2001; 2001WO-US01333.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0246476.
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PR 17-NOV-2000; 2000US-0249208.
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PR 17-NOV-2000; 2000US-0249210.
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PR 17-NOV-2000; 2000US-0249213.
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PR 17-NOV-2000; 2000US-0249216.


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QY 1976 ccgtgtcactccagcctcaagcaacagagcgagactccatctcaaaaaaaaaaaaaaa 2035
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QY 2036 aagaaaaaaa 2046
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Db 25015 ccaaaaaaaaa 25025

RESULT 14
AAK73222/c
ID AAK73222 standard; DNA: 15914 BP.
XX
AC AAK73222;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:28034.
XX
KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KM Cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN W0200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
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PR 31-JAN-2000; 2000US-0179065.
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 27, 2002, 11:29:53 ; Search time 5882.94 Seconds

(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	258.2	7.8	148846	2	AC008714	AC008714 Homo sapi
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		Noti.J.D., Johnson,A.K. and Dillon,J.D.					
		Structural and functional characterization of the leukocyte					
		integrin gene CD1d. Essential role of Spt and Sp3					
		J. Biol. Chem. 275 (12), 8959-8969 (2000)					
		MEDLINE					
		20187620					
		10722744					
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		Noti.J.D., Johnson,A.K. and Dillon,J.					
		Direct Submission					
		Submitted (16-SEP-1999) Molecular Biology, Guthrie Research					
		Institute, One Guthrie Square, Sayre, PA 18840, USA					

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CDS

Promoter
MRNA

BASE COUNT 2829 a 2838 c 3125 g 2757 t 8 others

ORIGIN

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OY	2221	ggatctcgtagggcccaatcccccaagtgcccgctgtccctcccaaccctcctgct	2273
Db	2221	ggatctcgtagggcccaatcccccaagtgcccgctgtccctcccaaccctcctcctgct	2273
RESULT 2			
AC093520			
LOCUS		169096 bp	DNA
DEFINITION		Homo sapiens chromosome 16 clone RP11-120K18, WORKING DRAFT	
ACCESSION		AC093520	
VERSION		AC093520.1	GI:15383809
KEYWORDS		HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
TITLE		1 (bases 1 to 169096)	
JOURNAL		DOE Joint Genome Institute.	
REFERENCE		Sequencing of Human Chromosome 16	
AUTHORS		Unpublished	
TITLE		2 (bases 1 to 169096)	
JOURNAL		DOE Joint Genome Institute.	
COMMENT		Submitted (31-AUG-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	
		-----Genome Center	
		Center: Joint Genome Institute	
		Center Code: JGI	
		Web site: http://www.jgi.doe.gov	

		Project Information	
		Center Project Name: 452703	
		Center clone name: RPc1-11_120K18	

		Summary Statistics	
		Consensus quality: 14729 bases at least Q40	
		Consensus quality: 157879 bases at least Q30	
		Consensus quality: 159986 bases at least Q20	
		Estimated insert size: 16300; agarose-rip estimation	
		Estimated insert size: 167296; sum-of-ovlgs estimation	

[illegible]

[illegible]

QY	1261	tgctcttccttgagtggttaagtgtggtggccagggtgtctgtgggagaaagctttgtagaggtctctga	1320
Db	160497	tgctttcttctgactggatgaatgtggggccacagggtctctggggaagaacctgttgagggtttctga	160556
QY	1321	ggagactccatctcvtggaaggcagagctcvtgggagctcvtgtgtcgtgtcccaaccaactcttatga	1380
Db	160557	ggggactccatctgaggagggacagagctcvtgggggctgtgtgtgtgtccgtccaacacactttatga	160616
QY	1381	ggaagctgaaggcaggggagtgcttcatgtgtcgagttgtgccggagtcagtagatgtgaact	1440
Db	160617	ggagctgagaggcagggagggagtgcttcaatgctcgaatgtgccggagttcagtagagttcactct	160676
QY	1441	gaatgaagaaggagctcagaaggctcvtgtctcagttgtgtgagctaaagctaacctctcagctgtgc	1500
Db	160677	gaattgaagaaggggcttcagggggctgtgtctctagatggcgactaaagcttacctctccagctggcc	160736
QY	1501	tatgtgtgtccagagcttccctcgtctcccaactatgagatccctcgtgtgtgtgtgaacagaagt	1560
Db	160737	ttatgtgtgtccacagagcttccctcgtctcccaactatgagatccctcgtgtgtgtgtgtgacacaggt	160796
QY	1561	ctcccccagagctcccccggagatgtggaaggtccaaagagccacagggagggaggaagtgtg	1620
Db	160797	cttcccccagagctcccccggagatgtggaaggtccaaagagccacagggagggaggaagtgtg	160856
QY	1621	gacatcacctccctctgtgagccttmmnnntttcccccagatccctgtactgcagtaggaagaagggc	1680
Db	160857	gacatcacctccctctgtgagccttmmnnntttcccccagatccctgtactgcagtaggaagaagggc	160913
QY	1681	ccccctcvtgaaaaactcgtacatcagaagttcaatltcaatcagttgcatcaaaaaatcaagcttgtctg	1740
Db	160914	ccccctcvtgaaaaactcgtacatcagaagttcaatltcaatcagttgcatcaaaaaatcaagcttgtgctg	160973
QY	1741	ggtgtcggtgtgtgtcattgacttataatcccaagactttgtggagggccgagaatgggtgtatcccc	1800
Db	160974	ggtgtcggtgtgtgtcattgacttataatcccaagactttgtggagggccgagaatgggtgtatcccc	161033
QY	1801	tgaagttcaaggaatttgtgtgacccagcctcvtggcacaacatgtgtbaaaaccccatctttacaaaaa	1860
Db	161034	tgaggtcagaggaatttgtgtgacccagcctcvtggcacaacatgtgtbaaaaccccatctttacaaaaa	161093
QY	1861	tataaaatatgacggggacatgtgtgtgctgtcacttgaatcccaagctactttggaagctga	1920
Db	161094	tt	161153
QY	1921	ggcagaagagatcgtcttgaaccacagagacaggaagtgtgcagtgtgagctcgaatcgtgtccgtt	1980
Db	161154	ggcagaagagatcgtcttgaaccacagagacaggaagtgtgcagtgtgagctcgaatcgtgtccgtt	161213
QY	1981	gcactccagcctcagcaacagagcgaagctcactctcaaaaaaataaaaaaataaaaaa	2040
Db	161214	gcactccagcctcagcaacagagcgaagctcactctcaaaaaaataaaaaaataaaaaaataaaaaa	161273
QY	2041	aaaaaagaanaaagaagcctcvtggaggtgtccctagaagatttggggctctcttaactcccaagctcc	2100
Db	161274	aaaaaagaanaaagaagcctcvtggaggtgtccctagaagatttggggctctcttttttttttttttttt	161333
QY	2101	ccggccacccaatatctcctcagctcctgtgtcttcttaacatgaagattcaaacctgtgtgtgag	2160
Db	161334	ccggccacccaatatctcctcagctcctgtgtgtcttcttaacatgaagattcaaacctgtgtgtgag	161393
QY	2161	gagcctacgacttctcagaagaatgcagagcgtcttvtgggcagagcgttgtgtcagttcgtt	2220
Db	161394	gagcctacgacttctcagaagaatgcagagcgtcttvtgggcagagcgttgtgtcagttcgtt	161453
QY	2221	ggatctcgtgtgtgtggcccaactcccccaagtgtccgcgtgtcttcccaacccctcgtt	2273
Db	161454	ggatctcgtgtgtgtgtggcccaactcccccaagtgtccgcgtgtcttcccaacccctcgtt	161506

LOCUS	DEFINITION	AC026471	189467 bp	DNA	linear	HTG 19-SEP-2001
AC026471/c	Homo sapiens chromosome 16 clone RP11-452L6, WORKING DRAFT					

[illegible]

```

Db 124101  GGATCTCGTAGAGCCCACTCCTCTTCCCACTCACTCAGT 124049
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RESULT 4
AC074302/c 100068 bp DNA linear HTG 04-OCT-2000
LOCUS
DEFINITION Homo sapiens chromosome 16q24.3 clone RP4-597612, WORKING DRAFT
AC074302
AC074302.1 GI:9454507
VERSION HTG; HTGS_PHASE2; HTGS_DRAFT.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 100068)
JOURNAL Kremenidictis,G., Gardner,A.E., Callen,D.F. and Sutherland,G.R.
TITLE Large Scale Sequencing of the Chromosome 16 region q24.3
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 100068)
Kremenidictis,G., Gardner,A.E., Callen,D.F., Mundt,M.O.,
Doggett,N.A. and Sutherland,G.R.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-2000) Cytoogenetics & Molecular Genetics, Women's
& Children's Hospital / Bionomics, 28 Dalgleish street Thebarton,
Adelaide, South Australia 5031, Australia
COMMENT
-----
Genome Centre : Cytoogenetics & Molecular Genetics
CMGCMCH
Website:http://www.wch.sa.gov.au/labmedic/genetics/sequencing.html
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 46155: contig of 46155 bp in length
* 46156 46612: gap of unknown length
* 46613 47595: contig of 983 bp in length
* 47596 48052: gap of unknown length
* 48053 49874: contig of 1822 bp in length
* 49875 50331: gap of unknown length
* 50332 52542: contig of 2211 bp in length
* 52543 52999: gap of unknown length
* 53000 53239: contig of 240 bp in length
* 53240 53696: gap of unknown length
* 53697 56256: contig of 8960 bp in length
* 56257 63112: gap of unknown length
* 63113 63696: contig of 584 bp in length
* 63697 64152: gap of unknown length
* 64153 66448: contig of 5296 bp in length
* 66449 69904: gap of unknown length
* 69905 70985: contig of 1081 bp in length
* 70986 71441: gap of unknown length
* 71442 72857: contig of 1416 bp in length
* 72858 73313: gap of unknown length
* 73314 79053: contig of 5740 bp in length
* 79054 79509: gap of unknown length
* 79510 80127: contig of 618 bp in length
* 80128 80583: gap of unknown length
* 80584 81893: contig of 1310 bp in length
* 81894 82349: gap of unknown length
* 82350 84298: contig of 1949 bp in length
* 84299 84754: gap of unknown length
* 84755 85366: contig of 612 bp in length
* 85367 85822: gap of unknown length
* 85823 86454: contig of 632 bp in length
* 86455 86910: gap of unknown length

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Db	27486	GRAGCCCAACATCTATTGTGGAGGCTGAGCGACGAAGAAGTCTCTTAAACCCAGGAGGTGAGG	27427
QY	1955	ttgcagcgagcgtcagatcgttcgcttgcactccagcctcagcaacagagcagactcat	2014
Db	27426	TTGCAGTGTGAGCTGAGATTTCCACACCTACCTCCAGCATGGCGACAAGATGATTTCCAT	27367
QY	2015	ctcaaaaaaaaaaaaaaaaaaaaaaaaaaagaagaagaagcgtggaggtctctggga	2073
Db	27366	CTCAAAAAACAAAAAACAACAAAAACAACAAAAAAMAATCAGGAGAGAAAGAGAGA	27308
RESULT	8		
AC011333/c			
LOCUS	AC011333	158326 bp	DNA linear HTG 23-APR-2001
DEFINITION	Homo sapiens chromosome 5 clone CTC-229L21, WORKING DRAFT SEQUENCE.		
ACCESSION	AC011333		
VERSION	AC011333.5	GI:8576050	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	DOE Joint Genome Institute.		
JOURNAL	Sequencing of Human Chromosome 5		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 158326)		
TITLE	DOE Joint Genome Institute.		
JOURNAL	Direct Submission		
COMMENT	Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
	On Jun 21, 2000 this sequence version replaced gi:1710596.		
	-----Genome Center		
	Center: Joint Genome Institute		
	Center Code: JGI		
	Web site: http://www.jgi.doe.gov		

	Project Information		
	Center Project Name: 273400, H309		
	Center clone name: CIT-HSPC_229L21		

	Summary Statistics		
	Consensus quality: 137047 bases at least Q40		
	Consensus quality: 148952 bases at least Q30		
	Consensus quality: 152398 bases at least Q20		
	Estimated insert size: 160000; pulse field gel estimation		
	Estimated insert size: 157126; sum-of-coverage estimation		
	Quality coverage: 6.32 in Q20 bases; pulse field gel estimation		
	Quality coverage: 6.43 in Q20 bases; sum-of-coverage estimation.		
	* NOTE: This is a 'working draft' sequence. It currently		
	* consists of 13 contigs. The true order of the pieces		
	* is not known and their order in this sequence record is		
	* arbitrary. Gaps between the contigs are represented as		
	* runs of N, but the exact sizes of the gaps are unknown.		
	* This record will be updated with the finished sequence		
	* as soon as it is available and the accession number will		
	* be preserved.		
	1		
	1304: contig of 1304 bp in length		
	1305		
	1404: gap of unknown length		
	2923: contig of 1519 bp in length		
	2924		
	3023: gap of unknown length		
	3024		
	4352: contig of 1329 bp in length		
	4353		
	4452: gap of unknown length		
	4453		
	6450: contig of 1998 bp in length		
	6451		
	6550: gap of unknown length		
	6551		
	8738: contig of 2188 bp in length		
	8739		
	8838: gap of unknown length		
	14240: contig of 5402 bp in length		
	14241		
	14340: gap of unknown length		
	14341		
	18104: contig of 3764 bp in length		
	18105		
	18204: gap of unknown length		
	25006: contig of 6802 bp in length		


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/clone.lib="RP11-11"
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159.200
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484.828
repeat_region
/rpt_family="L2"
1025.1073
repeat_region
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1095.1379
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1608.1662
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1700.1845
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/rpt_family="MERL_type"
1860.1966
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3461.3600
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4080.4483
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5898.5924
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6233.6331
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6332.6650
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7588.7621
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zc23c12.r1"
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10283.10398
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10575.10709
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11635.11816
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11813.11834
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(NID:g12687098)"
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repeat_region
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12115.12136

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13806.13855
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13856.14165
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14145.14193
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14166.14226
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14532.14563
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14564.14590
repeat_region
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14869.15080
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15082.15302
repeat_region
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15351.15643
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Query Match
 Best Local Similarity 7.8%; Score 257.2; DB 9; Length 209197;
 Matches 298; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

```

QY 1686 gctgaactgcatcagagtcacatcagtcgcatcaaaatcaggttgctgggtgc 1745
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47270 GCTGGATTGTAATCCCAAACTTTGCTGTCATTAATAAGACAACCTGGCCAGTGC 47329

QY 1746 ggtggctcatgttaatacccaagcacttgggaagcgagatgggcgtatccctgaag 1805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47330 GGTGGCTCACACCTATACCTCCAGCACTTGGAGGCTGAGGGGACAATACCTGAGG 47389

QY 1806 tcaggaagtttgaccagcctggccaacatggtgaacccacttaccaaaataaa 1865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47390 TTGGGAGTTTGAGATCAGCTGGCCAAATGTAAGAAACCCATCTTACTAAATACAA 47449

QY 1866 aatlagccggagatggtgcytgcactgttaatcccaagtaacttgggaagctgaagcaa 1925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47450 AATATGCCAGCATGTGTGCAGAGTGCCTGTATATCCAGTACTCGGAGGCTGAGGCAT 47509

QY 1926 gagaatcgcttgaacccaggaagagaaagtgcagtgagctgagatcgycgttcact 1985
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47510 GAAATCGCATGAACCCAGAGAGCGGAGGTGCAGTGAGCTGAGATCTCACCACTCCACT 47569

QY 1986 ccagcctcaagcaagcagagcagatcattcaaaaaaagaaaaaagaaaaa 2045
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47570 GCAAGCTGGGCAACAGAGAGACTCCTCATCAAAAAAAAAAAAAAAAAAAAAA 47629

QY 2046 agaaaa 2051
    |||
DB 47630 GACAAA 47635

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RESULT 10
 AL353705 166372 bp DNA linear PRI 30-JAN-2002
 LOCUS AL353705/c
 DEFINITION Human DNA sequence from clone RP11-336N8 on chromosome
 9q21.11-21.31, complete sequence.
 ACCESSION AL353705


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misc_feature      1..358
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repeat_region    /note="match: GSS: Em:AQ48911"
                  688..1876
repeat_region    /note="trigger3b repeat: matches 1..1231 of consensus"
                  1922..1970
repeat_region    /note="loop repeat: matches 181..229 of consensus"
                  1971..2277
repeat_region    /note="Alusx repeat: matches 1..307 of consensus"
                  2278..3194
repeat_region    /note="loop repeat: matches 229..1137 of consensus"
                  3198..3373
repeat_region    /note="loop repeat: matches 1049..1231 of consensus"
                  3374..3583
repeat_region    /note="TRIGER1 repeat: matches 2202..2418 of consensus"
                  3573..3723
repeat_region    /note="TRIGER1 repeat: matches 8..157 of consensus"
                  3731..3850
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                  3846..3879
repeat_region    /note="17 copies 2 mer at 91 conserved"
                  3954..3979
repeat_region    /note="13 copies 2 mer ac 92 conserved"
                  3976..4095
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                  4623..4742
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                  5416..5527
repeat_region    /note="2 copies 56 mer 88 conserved"
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                  7801..8089
repeat_region    /note="Aluy repeat: matches 1..289 of consensus"
                  complement(8343..8794)
misc_feature      /note="match: GSS: Em:B95656"
                  complement(8396..8658)
misc_feature      /note="match: GSS: Em:AQ105099"
                  8759..8932
repeat_region    /note="MIR repeat: matches 46..256 of consensus"
                  complement(9103..9576)
misc_feature      /note="match: GSS: Em:AQ053906"
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misc_feature      /note="match: STS: Em:G49329"
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                  14467..14599
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                  complement(16483..17160)
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repeat_region    /note="LIMC repeat: matches 1780..2100 of consensus"
                  complement(16943..17387)
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misc_feature      /note="match: GSS: Em:AQ791815"
                  17443..17860
repeat_region    /note="match: GSS: Em:AQ205149"
                  17563..17678
repeat_region    /note="MIR repeat: matches 25..144 of consensus"
                  18991..19084
repeat_region    /note="LIMC/D repeat: matches 5341..5439 of consensus"
                  19523..19695
repeat_region    /note="MIR1B repeat: matches 1..180 of consensus"
                  19696..19815
repeat_region    /note="Aluy repeat: matches 1..120 of consensus"
                  20646..21016
repeat_region    /note="THEIC repeat: matches 1..371 of consensus"
                  complement(22843..23225)
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                  complement(22893..23367)
misc_feature      /note="match: GSS: Em:AQ186295"
                  23350..23440
repeat_region    /note="LIMB3 repeat: matches 6696..6797 of consensus"
                  23659..23953
repeat_region    /note="Alusq repeat: matches 1..295 of consensus"
                  24062..24369
repeat_region    /note="Aluy repeat: matches 6..304 of consensus"
                  25270..25303
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                  25743..26120
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                  26324..26632
repeat_region    /note="AluyB8 repeat: matches 1..306 of consensus"
                  26696..26794
misc_feature      /note="3 copies 33 mer 85 conserved"
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                  27202..27781
misc_feature      /note="match: GSS: Em:B65034"
                  complement(30465..31019)
misc_feature      /note="match: GSS: Em:AQ506060"
                  31036..31580
misc_feature      /note="match: GSS: Em:AQ478810"
                  31106..31525
repeat_region    /note="match: GSS: Em:AQ094508"
                  31160..31363
repeat_region    /note="6 copies 34 mer 96 conserved"
                  31649..31747
repeat_region    /note="MIR repeat: matches 16..114 of consensus"
                  35121..35182
repeat_region    /note="MIR repeat: matches 119..183 of consensus"
                  35185..35437
misc_feature      /note="match: STS: Em:G49331"
                  35774..36190
repeat_region    /note="LIMB6 repeat: matches 5730..6173 of consensus"
                  36900..37167
misc_feature      /note="match: STS: Em:243443"
                  36995..37145
misc_feature      /note="match: STS: Em:G32626"
                  37284..37651
misc_feature      /note="match: STS: Em:G49332"
                  37591..37942
misc_feature      /note="match: STS: Em:G49333"

Query Match      7.8%; Score 255.8; DB 9; Length 56913;
```



```

----- Summary Statistics
Center project name: LB616
Center clone name: 815.1.9

Sequencing vector: M13; M77815; 56% of reads
Sequencing vector: Plasmid; n/a; 44% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 169944 bases at least Q40
Consensus quality: 171067 bases at least Q40
Consensus quality: 171612 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 172902; sum-of-connigs
Quality coverage: 8.6 in Q20 ba.
Quality coverage: 8.4 in Q20 ba.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

1
2053: contig of 2053 bp in length
2054 2153: gap of 100 bp
2154 6191: contig of 4038 bp in length
6192 6291: gap of 100 bp
6292 10482: contig of 4191 bp in length
10483 10582: gap of 100 bp
10583 14947: contig of 4365 bp in length
14948 15047: gap of 100 bp
15048 19581: contig of 4534 bp in length
19582 19681: gap of 100 bp
19682 33782: contig of 14101 bp in length
33783 33882: gap of 100 bp
33883 50444: contig of 16562 bp in length
50445 50544: gap of 100 bp
50545 74321: contig of 23777 bp in length
74322 74421: gap of 100 bp
74422 101256: contig of 26835 bp in length
101257 101356: gap of 100 bp
101357 135459: contig of 34103 bp in length
135460 135559: gap of 100 bp
135560 173902: contig of 38343 bp in length.

Location/Qualifiers
1. 173902
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17"
/clone="RP11-815r9"
/clone_lib="RPC1-11 Human Male BAC"
1. 2053
/note="Assembly-fragment
clone_end:SP6
vector_side:left"
2154. 6191
/note="assembly-fragment"
6292. 10482
/note="assembly-fragment"
10583. 14947
/note="assembly-fragment"
15048. 19581
/note="assembly-fragment"
19682. 33782
/note="assembly-fragment"
33883. 50444
/note="assembly-fragment"
50545. 74321
/note="assembly-fragment"
74422. 101256
/note="assembly-fragment"
101357. 135459
/note="assembly-fragment"

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misc.feature	135560..173902	/note="assembly_fragment"
Best Local Similarity	84.0%;	Pred. No. 2.7e-49;
Matches 288; Conservative	0; Mismatches 55; Indels 0; Gaps 0;	
Query Match	7.7%;	Score 255; DB 2; Length 173902;
Base COUNT	49143 a 35355 c 36175 g 52038 t 1011 others	
ORIGIN		
Db 1723	aaatcagcgtctggctgggtgctgcgtgctcgtatcatccagccacttgggaagc	1782
Db 2827	AAAGAAAAAAGAGCTGGGTGTGGTGGCTACCGCTGTAAATCCAGCACTTTGGAGGC	2886
Db 1783	cgaatggcgctatccctgaagctcaggaagttgtgacagcgttggccacatggtgaa	1842
Db 2887	TGAGGTAGGCGGATTAACCTAGAGCTCAGGAGTTTGAGACACGCTGGCCAACTGGTGAA	2946
Db 1843	ccccctcttaccataataataaattagccggcgatggtgctgcaattgtatccc	1902
Db 2947	CCCCATCTCTACTATAAAATACAAAATATAGCCGGGCATGTGACACACACCTGTATCCC	3006
Db 1903	agctactgggaagcgtgggcaagaatctgcgttaacccagagaagaaatcagtg	1962
Db 3007	AGCTACTAGAGAGGCTGAGCGCAGGAGAAATTCCTTAAGCCACGAGCGGAGGTTCCAGTG	3066
Db 1963	agctgagatcgtgcgctgtgcactcagcgtccagcacagcagagatccatccaaaa	2022
Db 3067	AGCTGAGATCATGTGCACCTGCACCTCCATCTGGCCAAAGAGTAGACACTGTGCTCAAAA	3126
Db 2023	aaaaaaaaaaaaaaaaaaaaaagaagagctggaggt 2065	
Db 3127	AAAAAAAAAAGAAAAAGAAAAAGAAAAAATAGTTTGTGT 3169	
RESULT 15		
LOCUS	HS215D11/c	
DEFINITION	HS215D11 12279 bp DNA linear PRI 23-NOV-1999	
DESCRIPTION	Human DNA sequence from clone 215D11 on chromosome 1p36.12-36.33 contains a gene for a RNA-binding protein regulatory subunit, a gene similar to rat gene 33, a pseudogene similar to PLA-X, ESTs, SRS, GSSs and Cpg islands, complete sequence.	
ACCESSION	AL034417.14 GI:5102616	
VERSION	AL034417.14	
KEYWORDS	HTG; Cpg Island.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	1 (bases 1 to 12279)	
TITLE	Wray, P.	
JOURNAL	Direct Submission	
COMMENT	Submitted (11-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 19, 1999 this sequence version replaced gi:5050947. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL, Sw, SWISSPROT, Tr, TREMBL This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu), where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.	

215D11 is from the human BAC library described in U-J. Kim et al. (1996) Genomics 34, 213-218. VECTOR: pBAC108L. IMPORTANT: This sequence is not the entire insert of clone 215D11. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true right end of clone 892F13 is at 100 in this sequence. This sequence was generated by the Sanger Centre from a human chromosome 1 bacterial clone contig constructed by Bedell J, G.S.C., St Louis, USA Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>.

FEATURES

source
1..122279
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="p36.12-36.33"
/clone="CTA-215D11"
/clone_lib="C11978SK-A1"
1..175
/note="Alusg/x repeat: matches 135. .309 of consensus"
repeat_region
897..2402
/note="SVA repeat: matches 340. .1386 of consensus"
misc_feature
1045..3435
/note="Cpg island"
/evidence="not_experimental"
1885
/note="weak data"
1934
/note="weak data"
2431..2569
/note="FLAM_C repeat: matches 1. .133 of consensus"
3681..3811
/note="L2 repeat: matches 2600. .2734 of consensus"
3862..4175
/note="Alusg repeat: matches 1. .310 of consensus"
4462..4592
/note="FLAM_A repeat: matches 1. .131 of consensus"
4981..5118
/note="HAL1 repeat: matches 1459. .1600 of consensus"
5758..6040
/note="Alusx repeat: matches 3. .291 of consensus"
6315..6582
/note="Aluo repeat: matches 28. .301 of consensus"
6713..7024
/note="Alusx repeat: matches 1. .312 of consensus"
7034..7330
/note="Alusg repeat: matches 1. .295 of consensus"
7384..7695
/note="Alusx repeat: matches 1. .312 of consensus"
7725..8034
/note="Alub repeat: matches 1. .312 of consensus"
8035..8621
/note="L1MA4 repeat: matches 5040. .5696 of consensus"
8622..8926
/note="Alusx repeat: matches 1. .306 of consensus"
8927..9289
/note="L1MA4 repeat: matches 5696. .6043 of consensus"
9299..9468
/note="MER84 repeat: matches 325. .508 of consensus"
9585..9691
/note="MER84 repeat: matches 1. .122 of consensus"
9692..9930
/note="L1MA4 repeat: matches 6054. .6292 of consensus"
9973..10052
/note="L2 repeat: matches 2659. .2732 of consensus"
10086..11010
/note="Cpg island"
/evidence="not_experimental"
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/gene="BK215D11.1"
/note="RNA-binding protein regulatory subunit"

match: cDNAs: Em:AF021819 Em:DB1380 Em:AJ007291
Em:AB015652
match: ESTs: Em:N77240 Em:AA186809 Em:AA315511 Em:AA305373
Em:AA129779 Em:AA082613 Em:J38029 Em:AA716183 Em:AA388672
Em:AA308838 Em:DB1064 Em:DB5402 Em:WA2607 Em:AA329174
Em:J35410 Em:AA312271
/product="BK215D11.1 (RNA-binding protein regulatory subunit)"
/evidence="not_experimental"
10536..34124
/gene="BK215D11.1"
join(11630..11719,14168..14269,18189..18248,19738..19807,26496..26582,33738..33898)
/gene="BK215D11.1"
/note="match: proteins: Tr:088767 Tr:014805 Tr:088306"
/codon_start=1
/evidence="not_experimental"
/product="BK215D11.1 (RNA-binding protein regulatory subunit)"
/protein_id="CAB52550.1"
/db_xref="GI:5731801"
/translation="MASKRALYILAKGAEETVIVDMRRAGIKVAVAGLADQPVQSRVVICPDASIEDARKRGGPDVYVPGNLGQNTSFAAYVEIKLEQENRGILIATCGPTALLAHEIGRSGSKVTTPLADKMMNGSHYTSERYEKDGLITSGPCTSFEEALIVEALNGKEVAQVAKAPLVLD"
11922..12202
/note="Alub repeat: matches 7. .297 of consensus"
12217..12518
/note="Alusg repeat: matches 1. .311 of consensus"
12664..12956
/note="Alusg1 repeat: matches 1. .294 of consensus"
13056..13257
/note="MIR repeat: matches 8. .241 of consensus"
13369..13641
/note="L1ME repeat: matches 5416. .5713 of consensus"
13938..14085
/note="FRAM repeat: matches -1. .146 of consensus"
14400..14477
/note="L2 repeat: matches 2606. .2692 of consensus"
14646..14832
/note="Alub repeat: matches 113. .308 of consensus"
15260..15564
/note="Aluo repeat: matches 1. .287 of consensus"
15641..16331
/note="L1MA5A repeat: matches 5587. .6294 of consensus"
16482..16772
/note="Aluo repeat: matches 2. .290 of consensus"
16872..17173
/note="Alusg repeat: matches 1. .307 of consensus"
17363..17660
/note="Alusx repeat: matches 1. .297 of consensus"
18429..18721
/note="Alusg repeat: matches 1. .294 of consensus"
18753..19053
/note="Aluo repeat: matches 1. .294 of consensus"
complement(19467..20068)
/note="match: GSS: Em:Bj152.1"
/evidence="not_experimental"
complement(join(19774..19807,26497..26582,33751..34091))
/note="match: STS: Em:G22443"
/evidence="not_experimental"
20495..20806
/note="Alusg repeat: matches 1. .312 of consensus"
21024..21313
/note="Aluo repeat: matches 1. .290 of consensus"
21314..21361
/note="Charlief repeat: matches 97. .147 of consensus"
21419..21468
/note="WADEI repeat: matches 32. .80 of consensus"
21471..21600
/note="Alusx repeat: matches 6. .138 of consensus"
21601..21899
/note="Alusg repeat: matches 1. .291 of consensus"

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repeat_region 21904..21995
/note="Charlie1 repeat: matches 2642..2758 of consensus"
repeat_region 22335..22587
/note="AlusG repeat: matches 60..312 of consensus"
repeat_region 22588..22769
/note="AlusX repeat: matches 116..298 of consensus"
repeat_region 22872..23189
/note="AluJ repeat: matches 1..300 of consensus"
repeat_region 23192..23506
/note="AluYB8 repeat: matches 1..316 of consensus"
repeat_region 23692..23997
/note="AlusG repeat: matches 1..307 of consensus"
repeat_region 23535..23863
/note="AluY repeat: matches 1..309 of consensus"
repeat_region 26302..26427
/note="FLAM_C repeat: matches 2..131 of consensus"
repeat_region 26595..26831
/note="AlusG/x repeat: matches 73..309 of consensus"
repeat_region 26830..27139
/note="AlusG repeat: matches 1..309 of consensus"
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Query Match

7.7%: Score 254.8; DB 9; Length 122279;

Best local Similarity 87.0%: Pred. No. 3e-49; Mismatches 42; Indels 0; Gaps 0;

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Matches 280; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1733 ctgagctgggtgcgctggtcctatgctataatccagcacttggaagccgaatgagc 1792
DB 46724 CTGGCTGGGTGCTGGCTCATGCTGTATCCAGACTTATAGGAGCGCCGAGCAGGT 46665

QY 1793 gtaaccctggaagtgaggtgtgtgacagcctggccaatgagtgaaacccatctt 1852
DB 46664 GGATCACTGACATTCAGAGTTTGAGACCAGCTGGCCAAATGATGTAACCTGTCTCT 46605

QY 1853 accaaataataaaatagccgggcatggtgagcactgtgtaataccagctacttg 1912
DB 46604 ACTAAAAATATACAAATATAGCTGGCATGTGGCGTGCACCTGTATCCAGCTACTAGG 46545

QY 1913 gaagctgaggcaagagaatcgctgaaaccagagagacggaagltgcagltgagctgagatc 1972
DB 46544 GAGGCTGAGGAGCAGAGATTCATTGAATCCAGAGCAGAGTTCAGAGTGAAGATT 46485

QY 1973 gtgacgttgacactccagcctcagcaacagagcgagactcctatctcaaaaaaaaaa 2032
DB 46484 GTGTCACTGCACTCCAGCTGGGAAACAAAGCAAGACTCATCTCAAAAAAAAAAAAAA 46425

QY 2033 aaaaagaaaaaaagaaaaaga 2054
DB 46424 AAAAAAGAAAGAAAAAAGA 46403
```

Search completed: September 27, 2002, 14:20:07
Job time: 10214 sec